RAW SEQUENCE LISTING PATENT APPLICATION US/08/612,661

DATE: 06/22/96 TIME: 13:24:28

INPUT SET: S11218.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

1			SEQUENCE LISTING	Does Not Comply	
3	(1) General Information:		:	Corrected Diskette Needed	
4 5 6 7 8	(i)	APPLICANT: Christensen, Frydenlund H Nielsen, Pet	ansen, Henrik	•	
9 10	(ii)	TITLE OF INVENTION: Sub	stituted Nucleic Ac	id Mimics	
11 12	(iii)	NUMBER OF SEQUENCES: 10		See	
13 14 15 16 17 18 19 20 21 22 23 24	, ,	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Woodcoc (B) STREET: One Libert (C) CITY: Philadelphia (D) STATE: PA (E) COUNTRY: USA (F) ZIP: 19103 COMPUTER READABLE FORM: (A) MEDIUM TYPE: Flopp (B) COMPUTER: IBM PC c (C) OPERATING SYSTEM:	y Place 46th. Floor y disk ompatible	See notes on attached pages	
25 26		(D) SOFTWARE: PatentIn		ion #1.30	
27 28 29 30 31	(vi)	CURRENT APPLICATION DAT (A) APPLICATION NUMBER (B) FILING DATE: 08-MA (C) CLASSIFICATION:	: US 08/612,661		
32 33 34 35 36	(viii)	ATTORNEY/AGENT INFORMAT (A) NAME: Caldwell, Jo (B) REGISTRATION NUMBE (C) REFERENCE/DOCKET N	hn W R: 28,937		
37 38 39 40 41	(ix)	TELECOMMUNICATION INFOR (A) TELEPHONE: 215-568 (B) TELEFAX: 215-568-3	-3100		

ERRORED SEQUENCES FOLLOW:

108

109

110 111

RAW SEQUENCE LISTING PATENT APPLICATION US/08/612,661

DATE: 06/22/96 TIME: 13:24:31

INPUT SET: S11218.raw 61 (2) INFORMATION FOR SEQ ID NO:2: 62 (i) SEQUENCE CHARACTERISTICS. 63 (A) LENGTH 17 amino acids 64 (B) TYPE: amino acid 65 nucleic acid (C) STRANDEDNESS: single 66 (D) TOPOLOGY: linear 67 68 (ii) MOLECULE TYPE: DNA (genomic) 69 70 accordingly. 71 (iii) HYPOTHETICAL: NO 72 73 (iv) ANTI-SENSE: YES 74 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: 76 10 77 GAGAGGAAAA --> 78 79 80 81 (2) INFORMATION FOR SEQ ID NO:3: 82 83 (i) SEQUENCE CHARACTERISTICS: 84 (A) LENGTH: 10 base pairs use-the-term "nucleix acid" 85 (B) TYPE: QNA (C) STRANDEDNESS: single 86 87 (D) TOPOLOGY: linear 88 89 (ii) MOLECULE TYPE: PNA C OK, here 90 91 (iii) HYPOTHETICAL: NO 92 93 (iv) ANTI-SENSE: YES 94 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 95 96 ->OK 97 TTTTCCTCTC 10 98 99 100 101 102 (2) INFORMATION FOR SEQ ID NO:4: 103 (i) SEQUENCE CHARACTERISTICS: 104 105 (A) LENGTH: 10 base pairs - nucleic add 106 (B) TYPE: (PNA) 107 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: PNA

RAW SEQUENCE LISTING PATENT APPLICATION US/08/612,661

DATE: 06/22/96 TIME: 13:24:35

			INDUM CEM CITATO
		(111) INDOMINATED AND	INPUT SET: S11218.raw
	112 113	(iii) HYPOTHETICAL: NO	
	113	(iv) ANTI-SENSE: YES	
	115	(IV) ANII-SENSE: IES	
	116	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
	117	(XI) DEGOUNCE DESCRIPTION. DEG ID NO.4.	
	118		
>	119	TTTTCNTCTC	10
•	120		
	121		
	122		
			· · · · · · · · · · · · · · · · · · ·
	123	(2) INFORMATION FOR SEQ ID NO:5:	
	124		
	125	(i) SEQUENCE CHARACTERISTICS:	
>	126	(A) LENGTH: 10 base pairs	
>	127	(B) TYPE: (PNA)	
	128	(C) STRANDEDNESS: single	
	129	(D) TOPOLOGY: linear	
	130 131	(ii) MOLECULE TYPE: PNA	
	131	(11) MOLECULE TYPE: PNA	
	132	(iii) HYPOTHETICAL: NO	
	134	(III) HIPOTHETICAL: NO	
	135	(iv) ANTI-SENSE: YES	
	136	(17) ANII BUNBU IUB	
	137	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
	138	(,	
	139		•
>o t	∠140	TTTTCNTNTC	10
	141		
	142		
	143		
	144	(2) INFORMATION FOR SEQ ID NO:6:	
	145	(2) Intolumiton toll buy 15 holds	
	146	(i) SEQUENCE CHARACTERISTICS:	
>	147	(A) LENGTH: 10 base pairs	
>	148	(B) TYPE: PNA	
	149	(C) STRANDEDNESS: single	
	150	(D) TOPOLOGY: linear	
	151		
	152	(ii) MOLECULE TYPE: PNA	•
	153		
	154	(iii) HYPOTHETICAL: NO	
	155		
	156	(iv) ANTI-SENSE: YES	
	157		
	158	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	-
_	159		••
>\$\		TTTTNNTCTC	10
	161 162		
	102		

RAW SEQUENCE LISTING PATENT APPLICATION US/08/612,661

DATE: 06/22/96 TIME: 13:24:38

INPUT SET: S11218.raw

	163		
	205	(2) INFORMATION FOR SEQ ID NO:9:	
	206	(2) INTORMATION FOR DEG ID HO. 3.	
	207	(i) SEQUENCE CHARACTERISTICS:	
	208	(A) LENGTH: 10 base pairs	
>	209	(B) TYPE PNA	
	210	(C) STRANDEDNESS: Single	
	211	(D) TOPOLOGY: linear	
	212	(b) for obodic finedi	
	213	(ii) MOLECULE TYPE: PNA	
	214	(II) MODECOED IIID. PAR	
	215	(iii) HYPOTHETICAL: NO	
	216	(III) MITOTREFICAL. NO	
	217	(iv) ANTI-SENSE: YES	
	218	(17) ANTI DENDE: 185	
	219	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
	220	(AI) DEGODACE DEBORITION. DEG ID NO. 3.	
	221	AGTCACCTAC	10
	222	no condition	10
	223		
	224		
	205	/AV TWOODY/MICH FOR GEO. TO WALLA	
	225	(2) INFORMATION FOR SEQ ID NO:10:	
	226	(i) GEOLIENGE GUADAGMEDIGEIGG	
	227 228	(i) SEQUENCE CHARACTERISTICS:	
>	228 229	(A) LENGTH: 10 base pairs (B) TYPE: RNA	
>	239	(C) STRANDEDNESS: single	
	230	(D) TOPOLOGY: linear	-
	231	(D) TOPOLOGI: Timeal	
	232	(ii) MOLEGULE MUDE, DNA	
	234	(ii) MOLECULE TYPE: PNA	
	235	(iii) HYPOTHETICAL: NO	
	236	(III) RIPOINEIICAL: NO	
	237	(iv) ANTI-SENSE: YES	
	238	(IA) WHII-SPHSE: IDS	
	239	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	·
	240	(YI) PEGORNOR DESCRIPTION: SEG ID NO:IO:	
	241		
	241	AGTCANCTAC	10
	242	AGI CANCIAC	10
	243		
	244		

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/612,661

DATE: 06/22/96 TIME: 13:24:41

INPUT SET: S11218.raw

Line	Error	Original Text	
64	Entered (17) and Calc. Seq. Length (0) differ	(A) LENGTH: 17 amino acids	
77	Wrong Amino Acid Designator	GAGAGGAAAA	10
84	Entered (10) and Calc. Seq. Length (0) differ	(A) LENGTH: 10 base pairs	
85	Wrong or Missing Sequence Type	(B) TYPE: PNA	
97	Wrong Amino Acid Designator	TTTTCCTCTC	10
105	Entered (10) and Calc. Seq. Length (0) differ	(A) LENGTH: 10 base pairs	
106	Wrong or Missing Sequence Type	(B) TYPE: PNA	
119	Wrong Amino Acid Designator	TTTTCNTCTC	10
126	Entered (10) and Calc. Seq. Length (0) differ	(A) LENGTH: 10 base pairs	
127	Wrong or Missing Sequence Type	(B) TYPE: PNA	
140	Wrong Amino Acid Designator	TTTTCNTNTC	10
147	Entered (10) and Calc. Seq. Length (0) differ	(A) LENGTH: 10 base pairs	
148	Wrong or Missing Sequence Type	(B) TYPE: PNA	
160	Wrong Amino Acid Designator	TTTTNNTCTC	10
209	Wrong or Missing Sequence Type	(B) TYPE: PNA	
229	Wrong or Missing Sequence Type	(B) TYPE: PNA	

08/6/2,66/

Notice of Availability

Applicant Aid for Biotechnology Computer Readable Form (CRF)
Sequence Listings Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (sequence rules: 37 CFR 1.821 through 1.825). (Final rules were published in the Federal Register (55 FR 18230) on May 1, 1990, and in the PTO Official Gazette (1114 Off.Gaz.PatOffice 29) on May 15, 1990.)

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software will be available via computer downloading (details below). Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO Official Gazette.

The software can be accessed/requested in the following locations:

- 1) Dial-up access to the Patent and Trademark Office Bulletin Board System.
 Phone number: 703-305-8950
 Cost: Free-of-charge
- Dial-up access through the Internet. FTP site: ftp.uspto.gov Login as "anonymous". Software is in directory /pub/checker Cost: Free-of-charge
- For diskette copies, telephone requests to 703-306-2600. Cost: \$25.00

For Further Information Contact: Meredith Beckhardt at 703-308-4212.